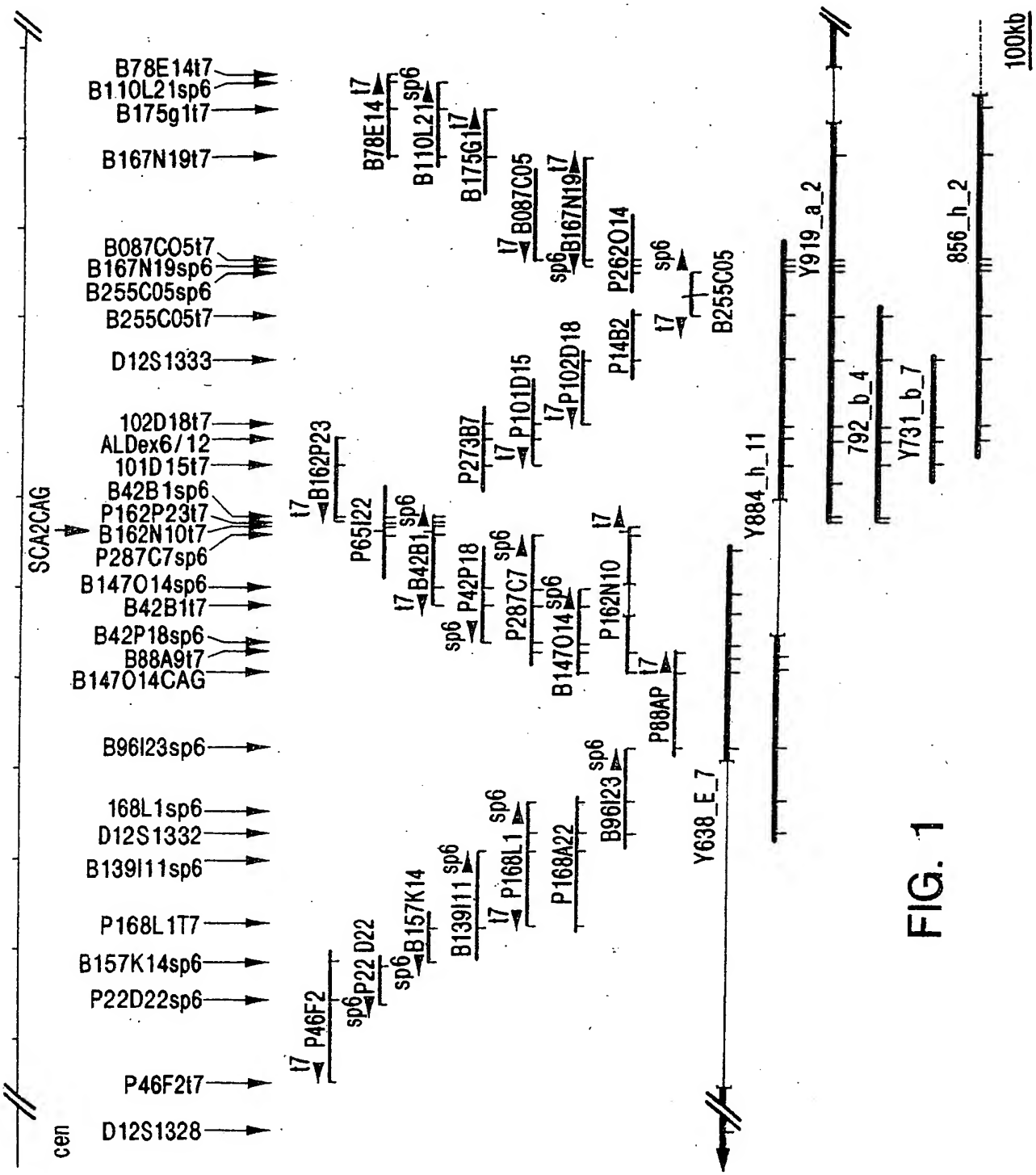
B78E14t7
B110L21sp6
B175g1t7
B167N19t7
B087C05t7
B167N19sp6
B255C05sp6
B255C05t7
D12S1333
102D18t7
ALDex6/12
101D15t7
B42B1sp6
P162P23t7
B162N10t7
P287C7sp6
B147O14sp6
B42B1t7
B42P18sp6
B88A9t7
B147O14CAG
B96I23sp6
168L1sp6
D12S1332
B139I11sp6
P168L1T7
B157K14sp6
P22D22sp6
P46F2t7
D12S1328
cen
SCA2CAG
B78E14
B110L21
B175G1
B087C05
B167N19
P262O14
B255C05
P14B2
P102D18
P101D15
P273B7
B162P23
P65I22
B42B1
P42P18
P287C7
B147O14
P162N10
P88AP
B96I23
P168A22
P168L1
B139I11
B157K14
P22D22
P46F2
Y638_E_7
Y884_h_11
Y919_a_2
792_b_4
Y731_b_7
856_h_2
100kb

FIG. 1

```
  1  TTGGTAGCAACGGAAACGGCGGCGGCGCGTTTCGGCCCGGCTCCCGGCGGCTCCTTGGTC

 61  TCGGCGGGCCTCCCCGCCCCTTCGTCGTCGTCCTTCTCCCCCTCGCCAGCCCGGGCGCCC

121  CTCCGGCCGCGCCAACCCGCGCCTCCCCGCTCGGCGCCCGTGCGTCCCCGCCGCGTTCCG

181  GCGTCTCCTTGGCGCGCCCGGCTCCCGGCTGTCCCCGCCCGGCGTGCGAGCCGGTGTATG
         SCA2-A
241  GGCCCCTCACCATGTCGCTGAAGCCCCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGC
                                                          SCA2-B
301  AGCAGCAACAGCAGCAGCAGCAGCAGCAGCAGCCGCCGCCCGCGGCTGCCAATGTCCGCA

361  AGCCCGGCGGCAGCGGCCTTCTAGCGTCGCCCGCCGCCGCGCCTTCGCCGTCCTCGTCCT

421  CGGTCTCCTCGTCCTCGGCCACGGCTCCCTCCTCGGTGGTCGCGGCGACCTCCGGCGGCG

481  GGAGGCCCGGCCTGGGCAG GTGGGTGTCGGCACCCC
```

FIG. 2

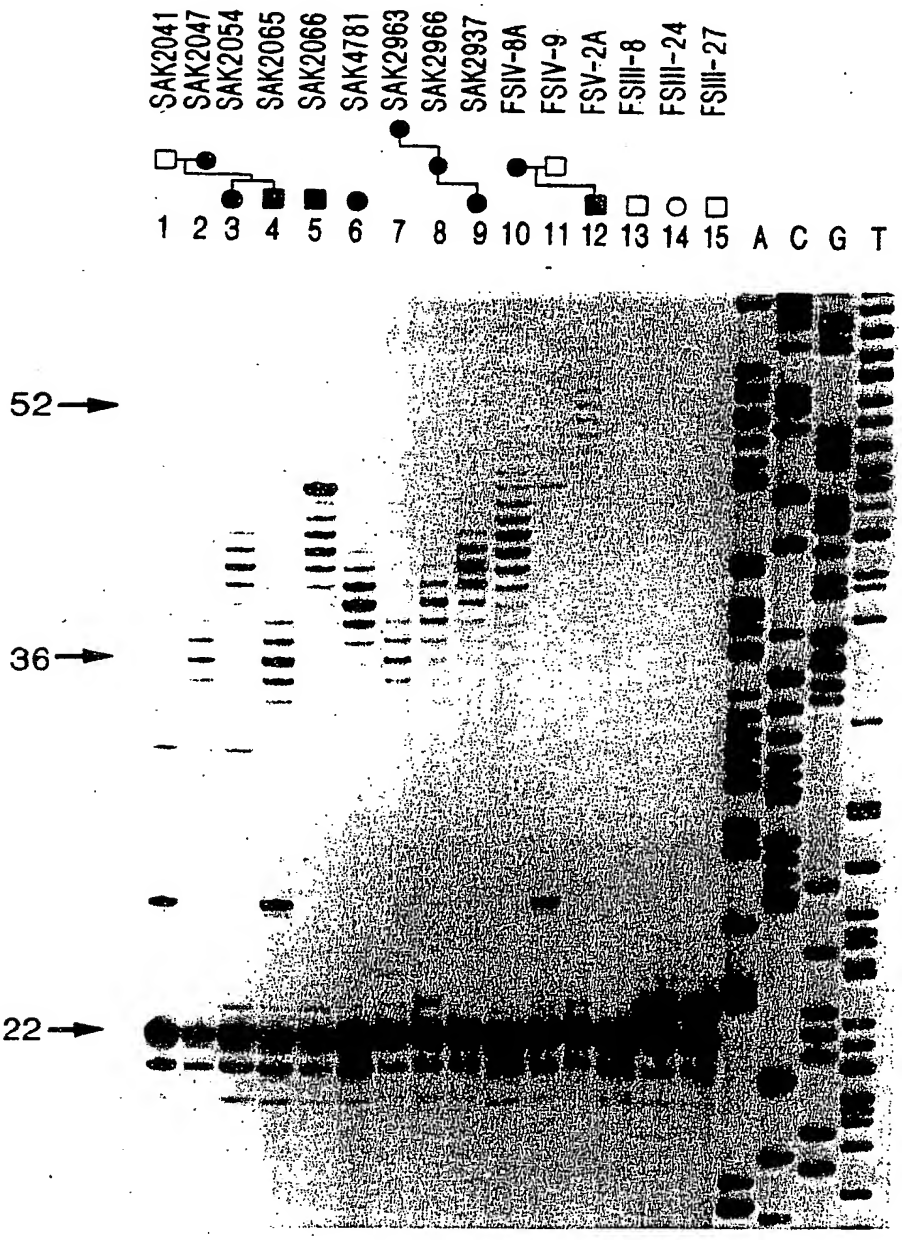

FIG. 3

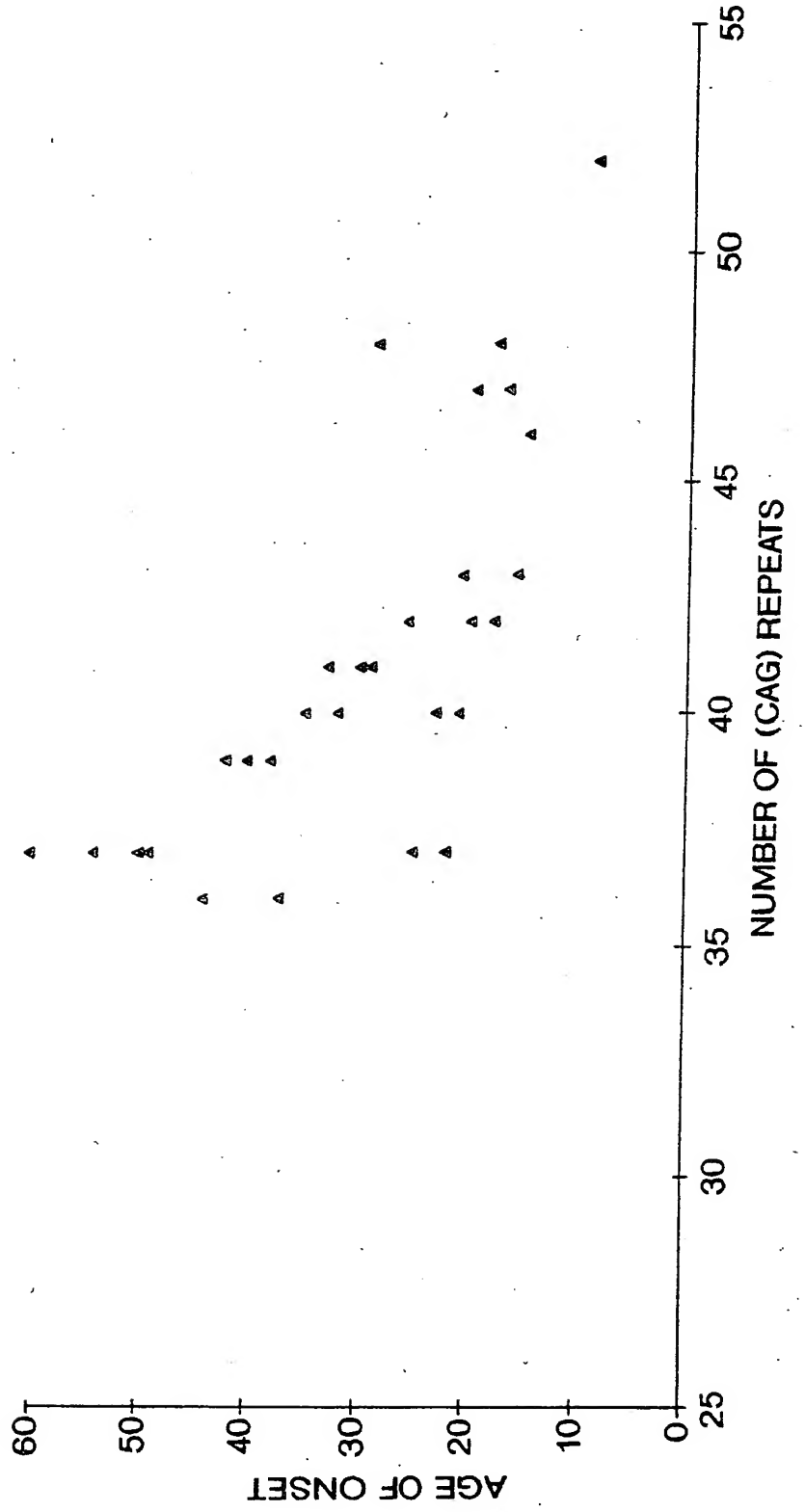
AGE OF ONSET
0
10
20
30
40
50
60
NUMBER OF (CAG) REPEATS
25
30
35
40
45
50
55

FIG. 4

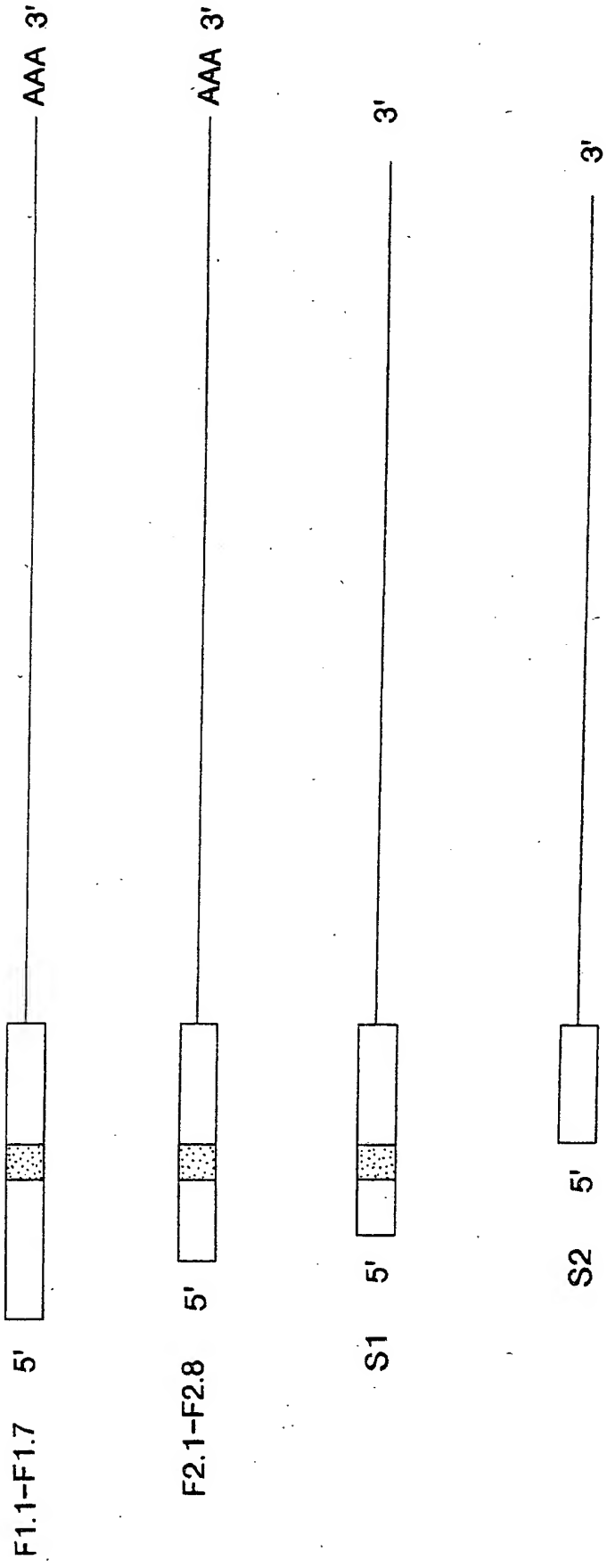

FIG. 5

```
   1 ACCCCCGAGAAAGCAACCCAGCGCGCCGCCCGCTCCTCACGTGTCCCTCCCGGCCCCGGG   60
  61 GCCACCTCACGTTCTGCTTCCGTCTGACCCCTCCGACTTCCGGTAAAGAGTCCCTATCCG  120
                                  *
 121 CACCTCCGCTCCCACCCGGCGCCTCGGCGCGCCCGCCCTCCGATGCGCTCAGCGGCCGCA  180
   1                                                 M  R  S  A  A  A    6
 181 GCTCCTCGGAGTCCCGCGGTGGCCACCGAGTCTCGCCGCTTCGCCGCAGCCAGGTGGCCC  240
   7 A  P  R  S  P  A  V  A  T  E  S  R  R  F  A  A  A  R  W  P     26
 241 GGGTGGCGCTCGCTCCAGCGGCCGGCGCGGCGGAGCGGGCGGGGCGGCGGTGGCGCGGCC  300
  27 G  W  R  S  L  Q  R  P  A  R  R  S  G  R  G  G  G  G  A  A     46
 301 CCGGGACCGTATCCCTCCGCCGCCCCTCCCCCGCCCGGCCCCGGCCCCCCTCCCTCCCGG  360
  47 P  G  P  Y  P  S  A  A  P  P  P  P  G  P  G  P  P  P  S  R     66
 361 CAGAGCTCGCCTCCCTCCGCCTCAGACTGTTTTGGTAGCAACGGCAACGGCGGCGGCGCG  420
  67 Q  S  S  P  P  S  A  S  D  C  F  G  S  N  G  N  G  G  G  A     86
 421 TTTCGGCCCGGCTCCCGGCGGCTCCTTGGTCTCGGCGGGCCTCCCCGCCCCTTCGTCGTC  480
  87 F  R  P  G  S  R  R  L  L  G  L  G  G  P  P  R  P  F  V  V    106
 481 GTCCTTCTCCCCCTCGCCAGCCCGGGCGCCCCTCCGGCCGCGCCAACCCGCGCCTCCCCG  540
 107 V  L  L  P  L  A  S  P  G  A  P  P  A  A  P  T  R  A  S  P    126
 541 CTCGGCGCCCGTGCGTCCCCGCCGCGTTCCGGCGTCTCCTTGGCGCGCCCGGCTCCCGGC  600
 127 L  G  A  R  A  S  P  P  R  S  G  V  S  L  A  R  P  A  P  G    146
                                        SCA2-A
 601 TGTCCCCGCCCGGCGTGCGAGCCGGTGTATGGGCCCCTCACCATGTCGCTGAAGCCCCAG  660
 147 C  P  R  P  A  C  E  P  V  Y  G  P  L  T  M  S  L  K  P  Q    166
 661 CAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAACAGCAGCAGCAGCAGCAGCAG  720
 167 Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q  Q    186
                                  SCA2-B
 721 CAGCCGCCGCCCGCGGCTGCCAATGTCCGCAAGCCCGGCGGCAGCGGCCTTCTAGCGTCG  780
 187 Q  P  P  P  A  A  A  N  V  R  K  P  G  G  S  G  L  L  A  S    206
 781 CCCGCCGCCGCGCCTTCGCCGTCCTCGTCCTCGGTCTCCTCGTCCTCGGCCACGGCTCCC  840
 207 P  A  A  A  P  S  P  S  S  S  S  V  S  S  S  S  A  T  A  P    226
 841 TCCTCGGTGGTCGCGGCGACCTCCGGCGGCGGGAGGCCCGGCCTGGGCAGAGGTCGAAAC  900
 227 S  S  V  V  A  A  T  S  G  G  G  R  P  G  L  G  R  G  R  N    246
 901 AGTAACAAAGGACTGCCTCAGTCTACGATTTCTTTTGATGGAATCTATGCAAATATGAGG  960
 247 S  N  K  G  L  P  Q  S  T  I  S  F  D  G  I  Y  A  N  M  R    266
 961 ATGGTTCATATACTTACATCAGTTGTTGGCTCCAAATGTGAAGTACAAGTGAAAAATGGA 1020
 267 M  V  H  I  L  T  S  V  V  G  S  K  C  E  V  Q  V  K  N  G    286
                                                        SCA2-14B
1021 GGTATATATGAAGGAGTTTTTAAAACTTACAGTCCGAAGTGTGATTTGGTACTTGATGCC 1080
 287 G  I  Y  E  G  V  F  K  T  Y  S  P  K  C  D  L  V  L  D  A    306
1081 GCACATGAGAAAAGTACAGAATCCAGTTCGGGGCCGAAACGTGAAGAAATAATGGAGAGT 1140
 307 A  H  E  K  S  T  E  S  S  S  G  P  K  R  E  E  I  M  E  S    326
1141 ATTTTGTTCAAATGTTCAGACTTTGTTGTGGTACAGTTTAAAGATATGGACTCCAGTTAT 1200
 327 I  L  F  K  C  S  D  F  V  V  V  Q  F  K  D  M  D  S  S  Y    346
1201 GCAAAAAGAGATGCTTTTACTGACTCTGCTATCAGTGCTAAAGTGAATGGCGAACACAAA 1260
 347 A  K  R  D  A  F  T  D  S  A  I  S  A  K  V  N  G  E  H  K    366
1261 GAGAAGGACCTGGAGCCCTGGGATGCAGGTGAACTCACAGCCAATGAGGAACTTGAGGCT 1320
 367 E  K  D  L  E  P  W  D  A  G  E  L  T  A  N  E  E  L  E  A    386
1321 TTGGAAAATGACGTATCTAATGGATGGGATCCCAATGATATGTTTCGATATAATGAAGAA 1380
 387 L  E  N  D  V  S  N  G  W  D  P  N  D  M  F  R  Y  N  E  E    406
1381 AATTATGGTGTAGTGTCTACGTATGATAGCAGTTTATCTTCGTATACAGTGCCCTTAGAA 1440
 407 N  Y  G  V  V  S  T  Y  D  S  S  L  S  S  Y  T  V  P  L  E    426
1441 AGAGATAACTCAGAAGAATTTTTAAAACGGGAAGCAAGGGCAAACCAGTTAGCAGAAGAA 1500
 427 R  D  N  S  E  E  F  L  K  R  E  A  R  A  N  Q  L  A  E  E    446
```

FIG. 6A

```
1501  ATTGAGTCAAGTGCCCAGTACAAAGCTCGAGTGGCCCTGGAAAATGATGATAGGAGTGAG  1560
 447  I  E  S  S  A  Q  Y  K  A  R  V  A  L  E  N  D  D  R  S  E   466
1561  GAAGAAAAATACACAGCAGTTCAGAGAAATTCCAGTGAACGTGAGGGGCACAGCATAAAC  1620
 467  E  E  K  Y  T  A  V  Q  R  N  S  S  E  R  E  G  H  S  I  N   486
1621  ACTAGGGAAAATAAATATATTCCTCCTGGACAAAGAAATAGAGAAGTCATATCCTGGGGA  1680
 487  T  R  E  N  K  Y  I  P  P  G  Q  R  N  R  E  V  I  S  W  G   506
1681  AGTGGGAGACAGAATTCACCGCGTATGGGCCAGCCTGGATCGGGCTCCATGCCATCAAGA  1740
 507  S  G  R  Q  N  S  P  R  M  G  Q  P  G  S  G  S  M  P  S  R   526
1741  TCCACTTCTCACACTTCAGATTTCAACCCGAATTCTGGTTCAGACCAAAGAGTAGTTAAT  1800
 527  S  T  S  H  T  S  D  F  N  P  N  S  G  S  D  Q  R  V  V  N   546
1801  GGAGGTGTTCCCTGGCCATCGCCTTGCCCATCTCCTTCCTCTCGCCCACCTTCTCGCTAC  1860
 547  G  G  V  P  W  P  S  P  C  P  S  P  S  S  R  P  P  S  R  Y   566
1861  CAGTCAGGTCCCAACTCTCTTCCACCTCGGGCAGCCACCCCTACACGGCCGCCCTCCAGG  1920
 567  Q  S  G  P  N  S  L  P  P  R  A  A  T  P  T  R  P  P  S  R   586
1921  CCCCCCTCGCGGCCATCCAGACCCCCGTCTCACCCCTCTGCTCATGGTTCTCCAGCTCCT  1980
 587  P  P  S  R  P  S  R  P  P  S  H  P  S  A  H  G  S  P  A  P   606
1981  GTCTCTACTATGCCTAAACGCATGTCTTCAGAAGGGCCTCCAAGGATGTCCCCAAAGGCC  2040
 607  V  S  T  M  P  K  R  M  S  S  E  G  P  P  R  M  S  P  K  A   626
2041  CAGCGACATCCTCGAAATCACAGAGTTTCTGCTGGGAGGGGTTCCATATCCAGTGGCCTA  2100
 627  Q  R  H  P  R  N  H  R  V  S  A  G  R  G  S  I  S  S  G  L   646
2101  GAATTTGTATCCCACAACCCACCCAGTGAAGCAGCTACTCCTCCAGTAGCAAGGACCAGT  2160
 647  E  F  V  S  H  N  P  P  S  E  A  A  T  P  P  V  A  R  T  S   666
2161  CCCTCGGGGGGAACGTGGTCATCAGTGGTCAGTGGGGTTCCAAGATTATCCCCTAAAACT  2220
 667  P  S  G  G  T  W  S  S  V  V  S  G  V  P  R  L  S  P  K  T   686
2221  CATAGACCCAGGTCTCCCAGACAGAACAGTATTGGAAATACCCCCAGTGGGCCAGTTCTT  2280
 687  H  R  P  R  S  P  R  Q  N  S  I  G  N  T  P  S  G  P  V  L   706
2281  GCTTCTCCCCAAGCTGGTATTATTCCAACTGAAGCTGTTGCCATGCCTATTCCAGCTGCA  2340
 707  A  S  P  Q  A  G  I  I  P  T  E  A  V  A  M  P  I  P  A  A   726
2341  TCTCCTACGCCTGCTAGTCCTGCATCGAACAGAGCTGTTACCCCTTCTAGTGAGGCTAAA  2400
 727  S  P  T  P  A  S  P  A  S  N  R  A  V  T  P  S  S  E  A  K   746
2401  GATTCCAGGCTTCAAGATCAGAGGCAGAACTCTCCTGCAGGGAATAAAGAAAATATTAAA  2460
 747  D  S  R  L  Q  D  Q  R  Q  N  S  P  A  G  N  K  E  N  I  K   766
2461  CCCAATGAAACATCACCTAGCTTCTCAAAAGCTGAAAACAAAGGTATATCACCAGTTGTT  2520
 767  P  N  E  T  S  P  S  F  S  K  A  E  N  K  G  I  S  P  V  V   786
2521  TCTGAACATAGAAAACAGATTGATGATTTAAAGAAATTTAAGAATGATTTTAGGTTACAG  2580
 787  S  E  H  R  K  Q  I  D  D  L  K  K  F  K  N  D  F  R  L  Q   806
2581  CCAAGTTCTACTTCTGAATCTATGGATCAACTACTAAACAAAAATAGAGAGGGAGAAAAA  2640
 807  P  S  S  T  S  E  S  M  D  Q  L  L  N  K  N  R  E  G  E  K   826
2641  TCAAGAGATTTGATCAAAGACAAAATTGAACCAAGTGCTAAGGATTCTTTCATTGAAAAT  2700
 827  S  R  D  L  I  K  D  K  I  E  P  S  A  K  D  S  F  I  E  N   846
2701  AGCAGCAGCAACTGTACCAGTGGCAGCAGCAAGCCGAATAGCCCCAGCATTTCCCCTTCA  2760
 847  S  S  S  N  C  T  S  G  S  S  K  P  N  S  P  S  I  S  P  S   866
2761  ATACTTAGTAACACGGAGCACAAGAGGGGACCTGAGGTCACTTCCCAAGGGGTTCAGACT  2820
 867  I  L  S  N  T  E  H  K  R  G  P  E  V  T  S  Q  G  V  Q  T   886
2821  TCCAGCCCAGCATGTAAACAAGAGAAAGACGATAAGGAAGAGAAGAAAGACGCAGCTGAG  2880
 887  S  S  P  A  C  K  Q  E  K  D  D  K  E  E  K  K  D  A  A  E   906
2881  CAAGTTAGGAAATCAACATTGAATCCCAATGCAAAGGAGTTCAACCCACGTTCCTTCTCT  2940
 907  Q  V  R  K  S  T  L  N  P  N  A  K  E  F  N  P  R  S  F  S   926
2941  CAGCCAAAGCCTTCTACTACCCCAACTTCACCTCGGCCTCAAGCACAACCTAGCCCATCT  3000
 927  Q  P  K  P  S  T  T  P  T  S  P  R  P  Q  A  Q  P  S  P  S   946
3001  ATGGTGGGTCATCAACAGCCAACTCCAGTTTATACTCAGCCTGTTTGTTTTGCACCAAAT  3060
 947  M  V  G  H  Q  Q  P  T  P  V  Y  T  Q  P  V  C  F  A  P  N   966
3061  ATGATGTATCCAGTCCCAGTGAGCCCAGGCGTGCAACCTTTATACCCAATACCTATGACG  3120
 967  M  M  Y  P  V  P  V  S  P  G  V  Q  P  L  Y  P  I  P  M  T   986
```

FIG. 6B

```
3121  CCCATGCCAGTGAATCAAGCCAAGACATATAGAGCAGTACCAAATATGCCCCAACAGCGG  3180
 987  P  M  P  V  N  Q  A  K  T  Y  R  A  V  P  N  M  P  Q  Q  R    1006
3181  CAAGACCAGCATCATCAGAGTGCCATGATGCACCCAGCGTCAGCAGCGGGCCCACCGATT  3240
1007  Q  D  Q  H  H  Q  S  A  M  M  H  P  A  S  A  A  G  P  P  I    1026
3241  GCAGCCACCCCACCAGCTTACTCCACGCAATATGTTGCCTACAGTCCTCAGCAGTTCCCA  3300
1027  A  A  T  P  P  A  Y  S  T  Q  Y  V  A  Y  S  P  Q  Q  F  P    1046
3301  AATCAGCCCCTTGTTCAGCATGTGCCACATTATCAGTCTCAGCATCCTCATGTCTATAGT  3360
1047  N  Q  P  L  V  Q  H  V  P  H  Y  Q  S  Q  H  P  H  V  Y  S    1066
3361  CCTGTAATACAGGGTAATGCTAGAATGATGGCACCACCAACACACGCCCAGCCTGGTTTA  3420
1067  P  V  I  Q  G  N  A  R  M  M  A  P  P  T  H  A  Q  P  G  L    1086
3421  GTATCTTCTTCAGCAACTCAGTACGGGGCTCATGAGCAGACGCATGCGATGTATGCATGT  3480
1087  V  S  S  S  A  T  Q  Y  G  A  H  E  Q  T  H  A  M  Y  A  C    1106
3481  CCCAAATTACCATACAACAAGGAGACAAGCCCTTCTTTCTACTTTGCCATTTCCACGGGC  3540
1107  P  K  L  P  Y  N  K  E  T  S  P  S  F  Y  F  A  I  S  T  G    1126
3541  TCCCTTGCTCAGCAGTATGCGCACCCTAACGCTACCCTGCACCCACATACTCCACACCCT  3600
1127  S  L  A  Q  Q  Y  A  H  P  N  A  T  L  H  P  H  T  P  H  P    1146
3601  CAGCCTTCAGCTACCCCCACTGGACAGCAGCAAAGCCAACATGGTGGAAGTCATCCTGCA  3660
1147  Q  P  S  A  T  P  T  G  Q  Q  Q  S  Q  H  G  G  S  H  P  A    1166
3661  CCCAGTCCTGTTCAGCACCATCAGCACCAGGCCGCCCAGGCTCTCCATCTGGCCAGTCCA  3720
1167  P  S  P  V  Q  H  H  Q  H  Q  A  A  Q  A  L  H  L  A  S  P    1186
3721  CAGCAGCAGTCAGCCATTTACCACGCGGGGCTTGCGCCAACTCCACCCTCCATGACACCT  3780
1187  Q  Q  Q  S  A  I  Y  H  A  G  L  A  P  T  P  P  S  M  T  P    1206
3781  GCCTCCAACACGCAGTCGCCACAGAATAGTTTCCCAGCAGCACAACAGACTGTCTTTACG  3840
1207  A  S  N  T  Q  S  P  Q  N  S  F  P  A  A  Q  Q  T  V  F  T    1226
3841  ATCCATCCTTCTCACGTTCAGCCGGCGTATACCAACCCACCCCACATGGCCCACGTACCT  3900
1227  I  H  P  S  H  V  Q  P  A  Y  T  N  P  P  H  M  A  H  V  P    1246
3901  CAGGCTCATGTACAGTCAGGAATGGTTCCTTCTCATCCAACTGCCCATGCGCCAATGATG  3960
1247  Q  A  H  V  Q  S  G  M  V  P  S  H  P  T  A  H  A  P  M  M    1266
3961  CTAATGACGACACAGCCACCCGGCGGTCCCCAGGCCGCCCTCGCTCAAAGTGCACTACAG  4020
1267  L  M  T  T  Q  P  P  G  G  P  Q  A  A  L  A  Q  S  A  L  Q    1286
4021  CCCATTCCAGTCTCGACAACAGCGCATTTCCCCTATATGACGCACCCTTCAGTACAAGCC  4080
1287  P  I  P  V  S  T  T  A  H  F  P  Y  M  T  H  P  S  V  Q  A    1306
4081  CACCACCAACAGCAGTTGTAAGGCTGCCCTGGAGGAACCGAAAGGCCAAATTCCCTCCTC  4140
1307  H  H  Q  Q  Q  L  *                                            1326
4141  CCTTCTACTGCTTCTACCAACTGGAAGCACAGAAAACTAGAATTTCATTTATTTTGTTTT  4200
4201  TAAAATATATATGTTGATTTCTTGTAACATCCAATAGGAATGCTAACAGTTCACTTGCAG  4260
4261  TGGAAGATACTTGGACCGAGTAGAGGCATTTAGGAACTTGGGGGCTATTCCATAATTCCA  4320
4321  TATGCTGTTTCAGAGTCCCGCAGGTACCCCAGCTCTGCTTGCCGAAACTGGAAGTTATTT  4380
4381  ATTTTTTAATAACCCTTGAAAGTCATGAACACATCAGCTAGCAAAAGAAGTAACAAGAGT  4440
4441  GATTCTTGCTGCTATTACTGCTAAAAAAAAAAAAAAAAAAA  4481
```

FIG. 6C

```
                1                                                    50
Ataxin-2        VYGPLTMSLK PQQQQQQQQQ QQQQQQQQQQ QQQPPPAAAN VRKPGGSGLL
Mouse Ataxin-2  HEGPLTMSLK PQPQ...... .......... ....PPAPAT GRKPGG.GLL
A2RP            ........LA PQPPPPQQHQ ER........ .......... ..........
     Consensus  --------L- PQ-------- ---------- ---------- ----------

               51                                                   100
Ataxin-2        ASPAAAPSPS SSSVSSSSAT APSSVVA... ATSGGGRPGL GRGRNSNKGL
Mouse Ataxin-2  SSPGAAP.AS AAVTSASVVP APAAPVASSS AAAGGGRPGL GRGRNSSKGL
A2RP            ..PGAAAIGS A......... .......... .......... .RGQSTGKGP
     Consensus  --P-AA---S ---------- ---------- ---------- -RG----KG-

              101                                                   150
Ataxin-2        PQSTISFDGI YANMRMVHIL TSVVGSKCEV QVKNGGIYEG VFKTYSPKCD
Mouse Ataxin-2  PQPTISFDGI YANVRMVHIL TSVVGSKCEV QVKNGGIYEG VFKTYSPKCD
A2RP            PQSPV.FEGV YNNSRMLHFL TAVVGSTCDV KVKNGTTYEG IFKTLSSKFE
     Consensus  PQ----F-G- Y-N-RM-H-L T-VVGS-C-V -VKNG--YEG -FKT-S-K--

              151                                                   200
Ataxin-2        LVLDAAHEKS TESSSGPKRE EIMESILFKC SDFVVVQFKD MDSSYAKRDA
Mouse Ataxin-2  LVLDAAHEKS TESSSGPKRE EIMESVLFKC SDFVVVQFKD TDSSYARRDA
A2RP            LAVDAVHRKA SEPAGGPRRE DIVDTMVFKP SDVMLVHFRN VDFNYATKDK
     Consensus  L--DA-H-K- -E---GP-RE -I-----FK- SD---V-F-- -D--YA--D-

              201                                                   250
Ataxin-2        FTDSAIS..A KVNGEHKEKD LEPWDAGELT ANEELEALEN DVSNGWDPND
Mouse Ataxin-2  FTDSALS..A KVNGEHKEKD LEPWDAGELT ASEELE.LEN DVSNGWDPND
A2RP            FTDSAIAMNS KVNGEHKEKV LQRWEGGD.S NSDDYD.LES DMSNGWDPNE
     Consensus  FTDSA----- KVNGEHKEK- L--W--G--- -------LE- D-SNGWDPN-

              251                                                   300
Ataxin-2        MFRYNEENYG VVSTYDSSLS SYTVPLERDN SEEFLKREAR ANQLAEEIES
Mouse Ataxin-2  MFRYNEENYG VVSTYDSSLS SYTVPLERDN SEEFLKREAR ANQLAEEIES
A2RP            MFKFNEENYG VKTTYDSSLS SYTVPLEKDN SEEFRQRELR AAQLAREIES
     Consensus  MF--NEENYG V--TYDSSLS SYTVPLE-DN SEEF--RE-R A-QLA-EIES

              301                                                   350
Ataxin-2        SAQYKARVAL ENDD.RSEEE KYTAVQRNSS EREGHSINTR ENKYIPPGQR
Mouse Ataxin-2  SAQYKARVAL ENDD.RSEEE KYTAVQRNCS DREGHGPNTR DNKYIPPGQR
A2RP            SPQYRLRIAM ENDDGRTEEE KHSAVQRQGS GRESPSLASR EGKYIP....
     Consensus  S-QY--R-A- ENDD-R-EEE K--AVQR--S -RE------R --KYIP----

              351
Ataxin-2        NR
Mouse Ataxin-2  NR
A2RP            ..
     Consensus  --
```

FIG. 7